







Antivirulence as a new antibacterial approach for chemotherapy Sonia Escaich

Bacterial resistance to antibiotics is an issue that has led to the search for new antibacterial approaches. Drugs targeting virulence is an alternative approach to treat infections due to resistant bacteria. There is extensive literature and knowledge in the field of bacterial pathogenesis and genomic determinant of virulence. As therapeutic targets, virulence factors have been primarily addressed in the vaccine field to prevent infection by specific pathogens. Recently novel strategies to identify virulence inhibitors have been numerous and several new compounds were recently reported. This review emphasizes the new virulence inhibitors that have shown a biological activity and have made a proof of concept that disarming bacteria lead to the inhibition of bacterial infection in experimental models in vivo. Moreover, some of these new antivirulence compounds are able to inhibit the virulence of different related pathogenic species, indicating that it is possible to target common virulence mechanisms. The progress reported recently with proof of concept for antivirulence molecules at the preclinical stages should allow the antivirulence concept to become a reality as a new antibacterial approach.

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Introduction

The increasing antibiotic resistance of most clinically relevant bacteria creates an urgent need for new antibacterial classes that are not affected by resistance mechanisms already present in the bacterial population [1,2].

Very few new antibiotics with new mechanisms of action have been found in the recent past [3,4,5,6,7]. The mechanisms of resistance spreading in pathogenic bacterial populations call for the inhibition of new bacterial targets [4,8,9,0,10]. The inhibition of virulence targets could bring new antibacterial molecules with radically new mechanisms of action and represent an innovative

therapeutic concept [11,12]. Virulence is defined as the relative capacity of a microbe to cause damage in a host.

Although this definition is simple, it does encompass a wide variety of bacterial functions such as the direct effectors of pathogenicity (e.g. toxins), and many of the functions that are not essential for basic metabolism (in vitro essential genes) that contribute to the establishment of an infection in the host and are validated by deletion mutants (essential in vivo).

Antivirulence compounds could have advantages over classic antibiotics in two key ways. Firstly, the targets or pathways that are inhibited: Rather than target genes that are essential for basic metabolism *in vitro*, the targets are essential functions for host/pathogen interactions, which allow bacterial multiplication in the host. Therefore, the selective pressure for viability of mutants potentially carrying a resistance genotype should be limited to the host tissues where and when the targeted virulence factor is indispensable for bacterial survival. Secondly, the specificity of the effect (i.e. activity against bacteria that are causing pathogenesis via dissemination in the host) should preserve the bacteria constitutive of the normal flora.

With genomics and the diverse *in vivo* gene expression technologies available [13,14,15] our knowledge of bacterial infection physiopathology is improving [16,17]. It has permitted the identification of many new genes and metabolic pathways essential for a bacterium to cause infection of the host. Of particular interest are the bacterial targets that are conserved in several pathogenic species. To establish an infection and produce a disease, pathogenic bacteria have developed different virulence mechanisms in order to colonize, disseminate, adapt to the various environments in the host, subvert host functions, invade the host tissues, and overcome host defenses [18]. These different stages of pathogenesis represent a variety of pharmacological targets for inhibitors.

Inhibition of adhesion and colonization

The literature has shown that the prevention of bacterial adhesion to host cells could be achieved by inhibition of pili formation. Peptide mimetics that were able to bind the PapD protein, a conserved chaperone for pilus assembly in uropathogenic *E. coli* were designed and these inhibitors induce a decrease piliation of the bacteria [19]. The bicylic-2 pyridone designed by RDD are inhibitors of PapD; they have large spectrum potential and no effect on bacterial growth. They are able *in vitro* to decrease the relative abundance of pili per cell, biofilm formation, and the adherence of UPEC to bladder cells [20].

Virstatin was found by HTS, it is an inhibitor of ToxT a regulator of Cholera toxin expression and of pilus assembly. In an experimental model of infection by V. cholerae, Virstatin was able to inhibit virulence factors expression and intestinal colonization [21].

The inhibition of type III secretion systems (T3SS) may block the colonization step since this system is used by the Gram-negative pathogens to inject effectors directly into the host cell. Many of the translocated effector proteins interfere with intrinsic eukaryotic host cell functions to enable internalization of the bacteria in the eukaryotic cell. T3SSs play essential roles in the virulence of a large spectrum of Gram-negative pathogens, including Chlamydia, Escherichia coli, Pseudomonas, Salmonella, Shigella, and Yersinia [22]. Specific inhibitors of conserved effectors of T3SS have been reported. Benzimidazole derivatives (developed by Parateck Inc.) are inhibitors of a transcription factor important for the T3SS regulation of virulence in Pseudomonas aeruginosa. They have no direct antibacterial activity in vitro, but in a mice pneumonia model of infection, treatments with these compounds increase the survival rate [23].

The salicylidene acylhydrazides (developed by Innate Pharmaceuticals) inhibit S. typhimurium T3SS activity. They can also inhibit the Y. pseudotuberculosis or C. trachomatis T3SS [24]. These new compounds prevent secretion of T3SS effectors, invasion of cultured epithelial cells, and enteritis in vivo [25,26].

A benzylidene benzohydrazide able to block the secretion of Yersinia Yop effectors by interfering with the activity of the T3SS apparatus was also shown to inhibit C. trachomatis intracellular development [27].

Inhibition of the secretion of cell surface proteins

Sortases are required for the pathogenesis of many different bacterial infections and owing to the high degree of conservation in Gram-positive bacteria has been considered a good pharmacological antivirulence target [28,29].

Inhibitors of sortase such as peptidomimetic molecules have been identified by HTS assays [30]. Diarylacrylonitriles inhibitors of Sortase A also exhibited potent inhibitory activity against S. aureus cell adhesion to fibronectin [31]. With flavonol inhibitors of S. aureus sortase an activity in the bacteria was demonstrated using the clumping assay to fibringen [32]. Recently, Aryl-amino ethyl ketones (AAEKs) were shown to inhibit the sortase enzyme of two different bacterial species S. aureus and B. antracis [33]. This result based on structural design has opened the way for inhibitors with a larger spectrum of activity.

Siderophores are essential for the virulence of pathogenic bacteria. Iron is a limiting nutrient in the blood, and bacteria have developed several siderophore mechanisms for iron uptake. A salicylsulfamoyl adenosine was found to inhibit an enzyme involved in siderophore biosynthesis in M. tuberculosis and Y. pestis. The inhibitor was shown to inhibit the growth of both bacterial species in iron limiting conditions [34°°].

Inhibition of regulatory bacterial function

To adapt to the environment, bacteria use a large array of regulatory pathways and some of them are potential targets for new inhibitors.

Quorum sensing (QS) is a complex regulatory network that governs the expression of a series of bacterial virulence factors in response to cell density or environment changes. In particular, QS influences the ability of bacteria to form complex surface-associated structures such as biofilm and the ability of bacteria to resist clearing by the innate immune system [35]. The signals for QS are molecules called autoinducer (AI), and the promising QS inhibitors (QSI) that block the AI signaling have been reported [36]. In Gram-negative bacteria, QS is mediated by homoserine lactone derivatives. Synthetic derivatives of natural furanones interfere with the QS signals; they decrease QS regulated gene expression in *P. aeruginosa* in mice [37]. Furanone derivatives are able to suppress OS in the lung of mice, to accelerate the bacterial clearance in the lung and to improve survival in mice infected by P. aeruginosa [38]. Other QSI such as the halogenated anthranilic acid analogs inhibit a biosynthesis step of QS, and disrupt QS dependent gene expression. These compounds restricted P. aeruginosa systemic dissemination and mortality in mice, without perturbing bacterial viability [39]. Treatment, with the QS inhibitor furanone C-30, of mice harboring implants colonized with P. aeruginosa accelerates the clearing of the implants [40]. Natural products such as patulin and penicillic acid were shown to be biologically active QSI that increased the sensitivity of bacterial biofilm to trobamycin. In a mouse pulmonary infection model, P. aeruginosa was more rapidly cleared from the mice that were treated with patulin compared with the placebo group [41].

In Gram-positive bacteria the QS signal is made of autoinducer peptides (AIPs) that control virulence factors expression and interaction with the immune system [42,43°]. S. aureus (like P. aeruginosa) modulates virulence factor expression through at least two OS systems that regulate one another (AgR and RAP) [44**]. Inhibition of the AgR regulation was obtained by AIP analogs that antagonize the binding of the AIP to its receptor the Agr C histidine kinase and block the activation of the Agr response and then inhibit the expression of the regulated virulence factors [45]. The QS inhibitor RNAIII-inhibiting peptide (RIP) has already been assessed in multiple animal models and has been found to have strong activity in preventing staphylococcal infections [46].

Antibodies that have been derived against the AI in S. aureus are able to decrease the expression of the proteins regulated by the OS effector AgR, without affecting in vitro viability; furthermore, the treatment with the antibodies decreases the skin injury in mice [47°°]. These results represent an important demonstration of the feasibility of QS inhibition as a new antibacterial approach.

However, interference with QS in S. epidermitis has been reported to enhance biofilm formation [43]. Clinical isolates of S. aureus variant with loss of Agr function were found in biofilm, and the correlation between S. aureus strains with decreased sensitivity to vancomycin and AgR phenotype has been reported [48,49]. In vivo QS activation appears necessary in high density actively growing cells, but for quiescent cells and biofilm formation, QS inactivation appears to be a prerequisite [35,50,51]. These studies indicate that the temporal shift in the expression of QS during the infectious process might represent a challenge to use QSI in the host.

Inhibition of the bacterial cell wall resistance to the innate immunity

The resistance of bacteria to the innate immunity components is mediated by several virulence mechanisms and allows dissemination of the infection in the host.

The components of the innate immunity are either circulating molecules or cells. The molecules are the complement factors, and the antibacterial peptides such as defensins, which could have bactericidal effects by direct interactions with the bacterium cell wall in dividing bacteria [52,53°]. The circulating phagocytes and the polymorphonuclear leukocytes (PMNs) are able to kill invading bacteria after activation by releasing lytic peptides or reactive oxygen species (ROS).

Capsular polysaccharides are protecting bacteria from immune recognition and killing by cell-mediated immunity. Other genes essential to protect the bacteria from the destruction of the membrane integrity by the immune system have been identified and now investigated as virulence targets in Gram-positive and Gram-negative species.

In Gram-negative bacteria the outer membrane serves as the first barrier encountered by peptides and effectors of innate immunity. Lipopolysaccharide (LPS) is the major component of the outer membrane of Gram-negative bacteria. LPS is a major determinant of pathogenicity in Gram-negative bacteria and has been shown to be necessary for resistance to cationic peptides and complement [56].

LPS molecules are negatively charged and consist of the lipid A and core oligosaccharides to which are attached the polysaccharides forming the O Antigens. LPS biosynthesis is a target for antibiotics, and new inhibitors of biosynthetic enzymes have been reported

The resistance to cationic peptide is linked to the modification of lipid A, in particular by the addition of aminoarabinose into lipid A to decrease the surface negative charges. The modifying enzyme PmRk/Arnt could be inhibited with small molecules [57°].

The conserved core LPS is necessary for virulence [58,59] and is composed of heptose (Figure 1). Inhibition of heptose biosynthesis appears as a good bacterial target for inhibitors owing to the high degree of conservation in this pathway in Gram-negative bacteria, and inhibitors were found in HTS assays [60]. In Mutabilis we have validated RfaE (a core LPS biosynthesis enzyme) as a good target for inhibition using mutants in pathogenic E. coli. The mutants were highly sensitive to the complement factors present in serum, fully avirulent in vivo but were still able to colonize the intestine of mice. Promising potent inhibitors of RfaE enzyme were found using HTS and will be developed to render the bacteria sensitive to complement [61].

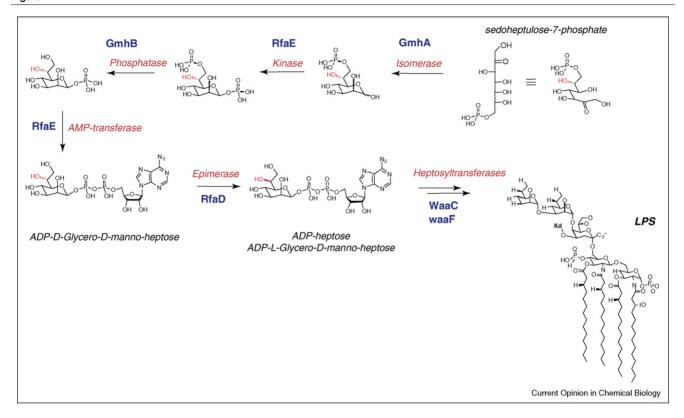
Among the many virulence factors described to be important for bacteria to resist, the innate immunity components are the mechanisms involved in resistance to cationic antimicrobial peptides (CAMP) [62]. The CAMP dominating targets are bacterial membranes, and CAMP interacts with the negatively charged bacterial surface. In Gram-positive pathogens, the antibacterial activities of the cationic peptides decrease as the bacterial electropositive charge surface increases [63,64].

Survival of bacteria to various bactericidal compounds including CAMP, cell killing, and cell invasion ability has been correlated to the D-alanylation of the lipotechoic acids (LTA) [65-67]. D-alanylation of LTA is mediated by the dlt operon (Figure 2) that is conserved in Grampositive species of medical importance such as the staphylococci and streptococci.

The role of the dlt operon for sensitivity to cationic peptides and virulence has led to considering dlt genes, in particular DltA, as good targets in the search to find inhibitors [67].

A substrate derivative of DltA (D-alanylacyl-sulfamoyladenosine) was found to be a potent inhibitor of the enzyme. When used in vitro the inhibitor was active in rendering different Bacillus subtilis strains more sensitive to vancomycin [68].

Figure 1



Heptose and inner core LPS biosynthesis in Gram-negative bacteria.

In Mutabilis, a series of potent inhibitors of S. agalactiae and S. pyogenes DltA was identified [69]. In vitro, the imidazolo-quinoxaline compound has no antibacterial activity by itself but was able to sensitize the bacteria

to the lytic effect of cationic peptides. The peptide used in this in vitro assay was colistin that mimics the effect of antibacterial cationic peptide. The bacterial growth inhibition observed in vitro in presence of colistin was

Figure 2

Scheme of D-alanylation of lipotechoic acids (LTA) in Gram-positive bacteria.

correlated to the inhibition of the target enzyme, as measured by the decreased amount of D-ala present in the LTA of the bacterial cell wall after incubation with the compound. In an experimental model of systemic infection of mice by S. agalactiae, the DltA inhibitors were able to affect the bacterial multiplication in the host, as shown by a dose dependent decrease of bacteremia. The in vivo antibacterial effects of the compounds were obtained at doses that are comparable to the effective doses of classic antibiotics [70]. These data represent a first proof of concept that an antivirulence molecule has an antibacterial effect in vivo by making the bacteria sensitive to host defenses.

Another proof of concept for an antivirulence molecule against S. aureus has been published recently [71**]. A specific virulence factor for S. aureus is staphyloxanthin a pigment with antioxidant activity necessary to protect the bacteria from the ROS produced by phagocytic defense of the host; a potent phosphosulfonate inhibitor of staphyloxanthin biosynthesis was shown to decrease bacteremia in a systemic model of infection in mice. These results demonstrate that it is possible to render the pathogenic S. aureus sensitive to innate immunity and obtain an antibacterial effect. However, the inhibition of the interaction with host immune defenses needs to be validated in the human host.

Conclusions

These given examples of new chemical entities active against virulence targets that are able to induce an in vivo antibacterial effect demonstrate that new drugs can

potentially be found to fight bacterial infections (Table 1). However, there are several issues for developing antivirulence drugs.

One of the main issues is the spectrum of activity. So the development of such drugs relies on the use of rapid diagnostic methods. With the availability of a large number of sequenced bacterial genomes, it is now possible to select virulence targets that are conserved in several species. Examples of such antivirulence inhibitors active on more than one species demonstrate the feasibility of this approach.

Another issue for the use of antivirulence molecules is the timing of expression of the virulence determinants during the infectious process. An ideal target would have a constitutive expression rather than inducible.

A main issue for drug discovery is the need for in vitro pharmacological assays to detect and optimize chemical inhibitors. Since virulence inhibitors by definition will not kill bacteria in vitro, functional assays should mimic the in vivo conditions necessary for the expression of the virulence phenotype and should be amenable to standardization. This key point is addressed in the selection of the virulence targets such as the resistance to soluble immune effectors such as CAMP or complement.

Potential indications will depend on the virulence mechanism targeted and on the spectrum of activity of the

Reference number	Name	Structure
[20]	Compound 2C	S CO ₂ Li
[21]	Virstatin	CO ₂ H
[23]	P005301	O ₂ N N N H

Table 1 (Continued) Reference number	Name	Structure
[24]	D9	HO Br
[27]	Compound 2	O ₂ N Br
[31]	Diarylacrylonitrile	MeO CN OMe
[33]	AAEK	S N
[34**]	AMS1	OH OO O
[39]	4CABA	CO ₂ H NH ₂
[41]	Patulin	HOO
[57 *]	Compound 1	CH ₃ OCO WOCOCH ₃
[61]	MUT2585	OMe N N OH

Table 1 (Continued) Reference number	Name	Structure
[68]	Sulfamoyl ը-ala	NH ₂ NH ₂ NH ₂ NH ₂ NH ₂
[71 °°]	BPH652	O

compounds. The choice would be based on the selective site of bacterial replication where the inhibition is needed (local or systemic).

For the molecules targeting the pili or the T3SS functions in enterobacteria, the clinical application would be to inhibit the bacterial multiplication at a specific site such as the intestine or the kidney.

For the antivirulence molecules addressing factors necessary for bacteria to avoid destruction by the immune system could be used to treat or prevent bacteremia.

With antivirulence compounds affecting the cell wall composition, the bacteria are also more sensitive to antibiotics, so combination therapy with current antibiotics could be envisioned.

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The paper presents important results demonstrating the validity of antivirulence as a new therapy against S. aureus.